

10/500796 #6

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SEQUENCE LISTING

<110> The Government of the United States of America, as represented by the Secretary, Department of Health and Human Services, Centers for Disease Control and Prevention

Chang, Gwong-Jen J

<120> Nucleic Acid Vaccines for Prevention of Flavivirus Infection

<130> 6395-64909-02

<150> PCT/US02/10764

<151> 2002-04-04

<150> 09/826,115

<151> 2001-04-04

<150> 09/701,536

<151> 2000-11-29

<150> PCT/US99/12298

<151> 1999-06-03

<150> 60/087,908

<151> 1998-06-04

<160> 61

<170> FastSEQ for Windows Version 4.0

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<223> Description of artificial sequence; note = synthetic construct

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<222> (25)...(48)

<221> misc_feature

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<210> 9

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 15 20 25

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Glu Asn Arg Cys Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu			
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gac act atc acg tac gaa tgt cct aag ctt acc atg ggc aat gat cca			1191
Asp Thr Ile Thr Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro			
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gag gat gtg gat tgc tgg tgt gac aac caa gaa gtc tac gtc caa tat			1239
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Ser Val Gln Thr His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala			
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Trp Leu Asp Ser Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn			
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Asn Arg Asp Phe Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu			
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Val Leu Glu Gly Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro			
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Thr Leu Asp Val Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu			
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Val Arg Ser Tyr Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val			
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<211> 697

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<223> pCDJE 2-7

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          35          40          45
Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly Glu Asn Arg Cys
          50          55          60
Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu Asp Thr Ile Thr
          65          70          75          80
Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro Glu Asp Val Asp
          85          90          95
Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr Gly Arg Cys Thr
          100         105         110
Arg Thr Arg His Ser Lys Arg Ser Arg Arg Ser Val Ser Val Gln Thr
          115         120         125
His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala Trp Leu Asp Ser
          130         135         140
Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn Trp Ile Ile Arg
          145         150         155         160
Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly Trp Met Leu Gly
          165         170         175
Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu Leu Leu Leu Val
          180         185         190
Ala Pro Ala Tyr Ser Phe Asn Cys Leu Gly Met Gly Asn Arg Asp Phe
          195         200         205
Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly

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210	215	220
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Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val Ala Arg Cys Pro		
	260	265
Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp Ser Ser Tyr Val		
	275	280
Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu		
	290	295
Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe Ser Cys Thr Ser		
305	310	315
Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile Lys Tyr Glu Val		
	325	330
Gly Ile Phe Val His Gly Thr Thr Thr Ser Glu Asn His Gly Asn Tyr		
	340	345
Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe Thr Val Thr Pro		
	355	360
Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr Gly Glu Val Thr		
	370	375
Leu Asp Cys Glu Pro Arg Ser Gly Leu Asn Thr Glu Ala Phe Tyr Val		
385	390	395
Met Thr Val Gly Ser Lys Ser Phe Leu Val His Arg Glu Trp Phe His		
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Asp Leu Ala Leu Pro Trp Thr Ser Pro Ser Ser Thr Ala Trp Arg Asn		
	420	425
Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala Thr Lys Gln Ser		
	435	440
Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His Gln Ala Leu Ala		
	450	455
Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys Leu Thr Ser Gly		
465	470	475
His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala Leu Lys Gly Thr		
	485	490
Thr Tyr Gly Met Cys Thr Glu Lys Phe Ser Phe Ala Lys Asn Pro Ala		
	500	505
Asp Thr Gly His Gly Thr Val Val Ile Glu Leu Ser Tyr Ser Gly Ser		
	515	520
		525

Asp Gly Pro Cys Lys Ile Pro Ile Ala Ser Val Ala Ser Leu Asn Asp		
530	535	540
Met Thr Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ala Thr		
545	550	555
Ser Ser Ala Ser Ser Lys Val Leu Val Glu Met Glu Pro Pro Phe Gly		
	565	570
Asp Ser Tyr Ile Val Val Gly Arg Gly Asp Lys Gln Ile Asn His His		
	580	585
Trp His Lys Ala Gly Ser Thr Leu Gly Lys Ala Phe Ser Thr Thr Leu		
	595	600
Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly Asp Thr Ala Trp Asp Phe		
	610	615
Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys Ala Val His Gln		
625	630	635
Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly Met Ser Trp Ile		
	645	650
		655

Thr	Gln	Gly	Leu	Met	Gly	Ala	Leu	Leu	Leu	Trp	Met	Gly	Val	Asn	Ala
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Arg	Asp	Arg	Ser	Ile	Ala	Leu	Ala	Phe	Leu	Ala	Thr	Gly	Gly	Val	Leu
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Val	Phe	Leu	Ala	Thr	Asn	Val	His	Ala							
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note =
 synthetic construct

<221> misc_feature
 <222> 1-46
 <223> WN 466

<400> 12
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<210> 13
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<210> 14
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 synthetic construct

<223> JE Signal

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<210> 15

<211> 5308
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
 synthetic construct

<221> CDS

<222> (911)...(2987)

<221> misc_feature

<222> (1)...(5308)

<223> pCBWN

<400> 15

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cgagcaaaat	ttaagctaca	acaaggcaag	gcttgaccga	caattgcatg	aagaatctgc	180
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gattattgac	tagttattaa	tagtaatcaa	ttacggggtc	attagttcat	agcccatata	300
tggagttccg	cgttacataa	cttacggtaa	atggcccggc	tggctgaccg	cccaacgacc	360
cccgccatt	gacgtcaata	atgacgtatg	ttcccatagt	aacgcccaata	gggactttcc	420
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atcatatgcc	aagtacgccc	cctattgacg	tcaatgacgg	taaatggccc	gcctggcatt	540
atgcccagta	catgacctta	tgggactttc	ctacttggca	gtacatctac	gtattagtca	600
tcgctattac	catggtgatg	cggttttttg	cagtacatca	atgggcgtgg	atagcggttt	660
gactcacggg	gatttccaag	tctccacccc	attgacgtca	atgggagttt	gttttggcac	720
caaaatcaac	gggactttcc	aaaatgtcgt	aacaactccg	ccccattgac	gcaaattgggc	780
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cgccgccgcc	atg ggc aag agg	tcc gcc ggc tca	atc atg tgg ctc	gcg		949
	Met Gly Lys Arg	Ser Ala Gly Ser	Ile Met Trp	Leu Ala		
	1	5	10			

agc ttg gca gtt gtc	ata gct tgt gca ggc gcc	gtg acc ctc tcg aac	997
Ser Leu Ala Val Val	Ile Ala Cys Ala Gly Ala	Val Thr Leu Ser Asn	
15	20	25	

ttc cag ggc aag gtg	atg atg acg gta aat gct	act gac gtc aca gat	1045
Phe Gln Gly Lys Val	Met Met Thr Val Asn Ala	Thr Asp Val Thr Asp	
30	35	40	45

gtc atc acg att cca	aca gct gct gga aag aac	cta tgc att gtc aga	1093
Val Ile Thr Ile Pro	Thr Ala Ala Gly Lys Asn	Leu Cys Ile Val Arg	
50	55	60	

gca atg gat gtg gga	tac atg tgc gat gat	act atc act tat gaa tgc	1141
Ala Met Asp Val Gly	Tyr Met Cys Asp Asp	Thr Ile Thr Tyr Glu Cys	
65	70	75	

cca gtg ctg tcg gct	ggt aat gat cca gaa	gac atc gac tgt tgg tgc	1189
Pro Val Leu Ser Ala	Gly Asn Asp Pro Glu	Asp Ile Asp Cys Trp Cys	
80	85	90	

aca aag tca gca gtc tac gtc agg tat gga aga tgc acc aag aca cgc	1237
Thr Lys Ser Ala Val Tyr Val Arg Tyr Gly Arg Cys Thr Lys Thr Arg	
95 100 105	
cac tca aga cgc agt cgg agg tca ctg aca gtg cag aca cac gga gaa	1285
His Ser Arg Arg Ser Arg Ser Leu Thr Val Gln Thr His Gly Glu	
110 115 120 125	
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Ser Thr Leu Ala Asn Lys Lys Gly Ala Trp Met Asp Ser Thr Lys Ala	
130 135 140	
aca agg tat ttg gta aaa aca gaa tca tgg atc ttg agg aac cct gga	1381
Thr Arg Tyr Leu Val Lys Thr Glu Ser Trp Ile Leu Arg Asn Pro Gly	
145 150 155	
tat gcc ctg gtg gca gcc gtc att ggt tgg atg ctt ggg agc aac acc	1429
Tyr Ala Leu Val Ala Ala Val Ile Gly Trp Met Leu Gly Ser Asn Thr	
160 165 170	
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Met Gln Arg Val Val Phe Val Val Leu Leu Leu Leu Val Ala Pro Ala	
175 180 185	
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Tyr Ser Phe Asn Cys Leu Gly Met Ser Asn Arg Asp Phe Leu Glu Gly	
190 195 200 205	
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Val Ser Gly Ala Thr Trp Val Asp Leu Val Leu Glu Gly Asp Ser Cys	
210 215 220	
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Val Thr Ile Met Ser Lys Asp Lys Pro Thr Ile Asp Val Lys Met Met	
225 230 235	
aat atg gag gcg gcc aac ctg gca gag gtc cgc agt tat tgc tat ttg	1669
Asn Met Glu Ala Ala Asn Leu Ala Glu Val Arg Ser Tyr Cys Tyr Leu	
240 245 250	
gct acc gtc agc gat ctc tcc acc aaa gct gcg tgc ccg acc atg gga	1717
Ala Thr Val Ser Asp Leu Ser Thr Lys Ala Ala Cys Pro Thr Met Gly	
255 260 265	
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Glu Ala His Asn Asp Lys Arg Ala Asp Pro Ala Phe Val Cys Arg Gln	
270 275 280 285	
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Gly Val Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys	
290 295 300	
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Gly Ser Ile Asp Thr Cys Ala Lys Phe Ala Cys Ser Thr Lys Ala Ile	
305 310 315	

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ctc cct tgg agc agt gct gga agt act gtg tgg agg aac aga gag acg Leu Pro Trp Ser Ser Ala Gly Ser Thr Val Trp Arg Asn Arg Glu Thr 415 420 425	2197
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ggc gtc tgt tca aag gct ttc aag ttt ctt ggg act ccc gcg gac aca Gly Val Cys Ser Lys Ala Phe Lys Phe Leu Gly Thr Pro Ala Asp Thr 495 500 505	2437
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Pro Val Gly Arg Leu Val Thr Val Asn Pro Phe Val Ser Val Ala Thr	
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Ala Asn Ala Lys Val Leu Ile Glu Leu Glu Pro Pro Phe Gly Asp Ser	
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<210> 16

<211> 692

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<223> pCBWN

<400> 16

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Lys Val Met Thr Val Asn Ala Thr Asp Val Thr Asp Val Ile Thr
35     40     45
Ile Pro Thr Ala Ala Gly Lys Asn Leu Cys Ile Val Arg Ala Met Asp
50     55     60
Val Gly Tyr Met Cys Asp Asp Thr Ile Thr Tyr Glu Cys Pro Val Leu
65     70     75     80
Ser Ala Gly Asn Asp Pro Glu Asp Ile Asp Cys Trp Cys Thr Lys Ser
85     90     95
Ala Val Tyr Val Arg Tyr Gly Arg Cys Thr Lys Thr Arg His Ser Arg
100    105    110
Arg Ser Arg Arg Ser Leu Thr Val Gln Thr His Gly Glu Ser Thr Leu
115    120    125
Ala Asn Lys Lys Gly Ala Trp Met Asp Ser Thr Lys Ala Thr Arg Tyr
130    135    140
Leu Val Lys Thr Glu Ser Trp Ile Leu Arg Asn Pro Gly Tyr Ala Leu
145    150    155    160

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Asn	Cys	Leu	Gly	Met	Ser	Asn	Arg	Asp	Phe	Leu	Glu	Gly	Val	Ser	Gly
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	210					215					220				
Met	Ser	Lys	Asp	Lys	Pro	Thr	Ile	Asp	Val	Lys	Met	Met	Asn	Met	Glu
225					230					235					240
Ala	Ala	Asn	Leu	Ala	Glu	Val	Arg	Ser	Tyr	Cys	Tyr	Leu	Ala	Thr	Val
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Ser	Asp	Leu	Ser	Thr	Lys	Ala	Ala	Cys	Pro	Thr	Met	Gly	Glu	Ala	His
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Asn	Asp	Lys	Arg	Ala	Asp	Pro	Ala	Phe	Val	Cys	Arg	Gln	Gly	Val	Val
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305					310					315					320
Ile	Leu	Lys	Glu	Asn	Ile	Lys	Tyr	Glu	Val	Ala	Ile	Phe	Val	His	Gly
			325						330					335	
Pro	Thr	Thr	Val	Glu	Ser	His	Gly	Asn	Tyr	Ser	Thr	Gln	Val	Gly	Ala
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Thr	Gln	Ala	Gly	Arg	Phe	Ser	Ile	Thr	Pro	Ala	Ala	Pro	Ser	Tyr	Thr
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Leu	Lys	Leu	Gly	Glu	Tyr	Gly	Glu	Val	Thr	Val	Asp	Cys	Glu	Pro	Arg
	370					375					380				
Ser	Gly	Ile	Asp	Thr	Asn	Ala	Tyr	Tyr	Val	Met	Thr	Val	Gly	Thr	Lys
385					390					395					400
Thr	Phe	Leu	Val	His	Arg	Glu	Trp	Phe	Met	Asp	Leu	Asn	Leu	Pro	Trp
			405						410					415	
Ser	Ser	Ala	Gly	Ser	Thr	Val	Trp	Arg	Asn	Arg	Glu	Thr	Leu	Met	Glu
		420						425					430		
Phe	Glu	Glu	Pro	His	Ala	Thr	Lys	Gln	Ser	Val	Ile	Ala	Leu	Gly	Ser
	435						440					445			
Gln	Glu	Gly	Ala	Leu	His	Gln	Ala	Leu	Ala	Gly	Ala	Ile	Pro	Val	Glu
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465					470					475					480
Val	Lys	Met	Glu	Lys	Leu	Gln	Leu	Lys	Gly	Thr	Thr	Tyr	Gly	Val	Cys
			485						490					495	
Ser	Lys	Ala	Phe	Lys	Phe	Leu	Gly	Thr	Pro	Ala	Asp	Thr	Gly	His	Gly
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Thr	Val	Val	Leu	Glu	Leu	Gln	Tyr	Thr	Gly	Thr	Asp	Gly	Pro	Cys	Lys
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Phe Arg Ser Leu Phe Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Leu				
	645		650	655
Gly Ala Leu Leu Trp Met Gly Ile Asn Ala Arg Asp Arg Ser Ile				
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Asn Val His Ala				
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<210> 17

<211> 5334

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> CDS

<222> (916)...(3007)

<221> misc_feature

<222> (1)...(5334)

<223> pCBE 1-14

<400> 17

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ggc tca atc atg tgg ctc gcg agc ttg gca gtt gtc ata gct tgt gcg	999
Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala	
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Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys Leu Leu Met Thr Ile	
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Asn Asn Thr Asp Ile Ala Asp Val Ile Val Ile Pro Thr Ser Lys Gly	
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Glu Asn Arg Cys Trp Val Arg Ala Ile Asp Val Gly Tyr Met Cys Glu	
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Asp Thr Ile Thr Tyr Glu Cys Pro Lys Leu Thr Met Gly Asn Asp Pro	
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Glu Asp Val Asp Cys Trp Cys Asp Asn Gln Glu Val Tyr Val Gln Tyr	
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Ser Val Gln Thr His Gly Glu Ser Ser Leu Val Asn Lys Lys Glu Ala	
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Trp Leu Asp Ser Thr Lys Ala Thr Arg Tyr Leu Met Lys Thr Glu Asn	
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Trp Ile Ile Arg Asn Pro Gly Tyr Ala Phe Leu Ala Ala Val Leu Gly	
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Trp Met Leu Gly Ser Asn Asn Gly Gln Arg Val Val Phe Thr Ile Leu	
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Asn Arg Asp Phe Ile Glu Gly Ala Ser Gly Ala Thr Trp Val Asp Leu	
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Val Leu Glu Gly Asp Ser Cys Leu Thr Ile Met Ala Asn Asp Lys Pro	
225 230 235	
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Thr Leu Asp Val Arg Met Ile Asn Ile Glu Ala Ser Gln Leu Ala Glu	
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gtc aga agt tac tgc tat cat gct tca gtc act gac atc tcg acg gtg	1719
Val Arg Ser Tyr Cys Tyr His Ala Ser Val Thr Asp Ile Ser Thr Val	
255 260 265	

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Ala Arg Cys Pro Thr Thr Gly Glu Ala His Asn Glu Lys Arg Ala Asp	
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Ser Ser Tyr Val Cys Lys Gln Gly Phe Thr Asp Arg Gly Trp Gly Asn	
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Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Asp Thr Cys Ala Lys Phe	
305 310 315	
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Ser Cys Thr Ser Lys Ala Ile Gly Arg Thr Ile Gln Pro Glu Asn Ile	
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Lys Tyr Glu Val Gly Ile Phe Val His Gly Thr Thr Thr Ser Glu Asn	
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His Gly Asn Tyr Ser Ala Gln Val Gly Ala Ser Gln Ala Ala Lys Phe	
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Thr Val Thr Pro Asn Ala Pro Ser Ile Thr Leu Lys Leu Gly Asp Tyr	
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gcg tgg aga aac aga gaa ctc ctc atg gaa ttt gaa gag gcg cac gcc	2247
Ala Trp Arg Asn Arg Glu Leu Leu Met Glu Phe Glu Glu Ala His Ala	
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aca aaa cag tcc gtt gtt gct ctt ggg tca cag gaa gga ggc ctc cat	2295
Thr Lys Gln Ser Val Val Ala Leu Gly Ser Gln Glu Gly Gly Leu His	
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Gln Ala Leu Ala Gly Ala Ile Val Val Glu Tyr Ser Ser Ser Val Lys	
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Leu Thr Ser Gly His Leu Lys Cys Arg Leu Lys Met Asp Lys Leu Ala	

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gcc tgg gac ttt ggc tct att gga ggg gtc ttc aac tcc ata gga aaa Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile Gly Lys 625 630 635			2823
gcc gtt cac caa gtg ttt ggt ggt gcc ttc aga aca ctc ttt ggg gga Ala Val His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly 640 645 650			2871
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<211> 697

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<223> pCBE 1-14

<400> 18

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Leu	Ser	Asn	Phe	Gln	Gly	Lys	Leu	Leu	Met	Thr	Ile	Asn	Asn	Thr	Asp
		35					40					45			

Ile	Ala	Asp	Val	Ile	Val	Ile	Pro	Thr	Ser	Lys	Gly	Glu	Asn	Arg	Cys
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Trp	Val	Arg	Ala	Ile	Asp	Val	Gly	Tyr	Met	Cys	Glu	Asp	Thr	Ile	Thr
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Tyr	Glu	Cys	Pro	Lys	Leu	Thr	Met	Gly	Asn	Asp	Pro	Glu	Asp	Val	Asp
				85					90					95	
Cys	Trp	Cys	Asp	Asn	Gln	Glu	Val	Tyr	Val	Gln	Tyr	Gly	Arg	Cys	Thr
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Arg	Thr	Arg	His	Ser	Lys	Arg	Ser	Arg	Arg	Ser	Val	Ser	Val	Gln	Thr
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His	Gly	Glu	Ser	Ser	Leu	Val	Asn	Lys	Lys	Glu	Ala	Trp	Leu	Asp	Ser
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Thr	Lys	Ala	Thr	Arg	Tyr	Leu	Met	Lys	Thr	Glu	Asn	Trp	Ile	Ile	Arg
145					150					155					160
Asn	Pro	Gly	Tyr	Ala	Phe	Leu	Ala	Ala	Val	Leu	Gly	Trp	Met	Leu	Gly
				165					170					175	
Ser	Asn	Asn	Gly	Gln	Arg	Val	Val	Phe	Thr	Ile	Leu	Leu	Leu	Leu	Val
			180					185					190		
Ala	Pro	Ala	Tyr	Ser	Phe	Asn	Cys	Leu	Gly	Met	Gly	Asn	Arg	Asp	Phe
		195					200					205			
Ile	Glu	Gly	Ala	Ser	Gly	Ala	Thr	Trp	Val	Asp	Leu	Val	Leu	Glu	Gly
	210					215					220				
Asp	Ser	Cys	Leu	Thr	Ile	Met	Ala	Asn	Asp	Lys	Pro	Thr	Leu	Asp	Val
225					230					235					240
Arg	Met	Ile	Asn	Ile	Glu	Ala	Ser	Gln	Leu	Ala	Glu	Val	Arg	Ser	Tyr
			245						250					255	
Cys	Tyr	His	Ala	Ser	Val	Thr	Asp	Ile	Ser	Thr	Val	Ala	Arg	Cys	Pro
			260					265					270		
Thr	Thr	Gly	Glu	Ala	His	Asn	Glu	Lys	Arg	Ala	Asp	Ser	Ser	Tyr	Val
		275					280					285			
Cys	Lys	Gln	Gly	Phe	Thr	Asp	Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Leu
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Phe	Gly	Lys	Gly	Ser	Ile	Asp	Thr	Cys	Ala	Lys	Phe	Ser	Cys	Thr	Ser
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Lys	Ala	Ile	Gly	Arg	Thr	Ile	Gln	Pro	Glu	Asn	Ile	Lys	Tyr	Glu	Val
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385					390					395					400
Met	Thr	Val	Gly	Ser	Lys	Ser	Phe	Leu	Val	His	Arg	Glu	Trp	Phe	His
			405						410					415	
Asp	Leu	Ala	Leu	Pro	Trp	Thr	Ser	Pro	Ser	Ser	Thr	Ala	Trp	Arg	Asn
		420						425					430		
Arg	Glu	Leu	Leu	Met	Glu	Phe	Glu	Glu	Ala	His	Ala	Thr	Lys	Gln	Ser
		435					440					445			
Val	Val	Ala	Leu	Gly	Ser	Gln	Glu	Gly	Gly	Leu	His	Gln	Ala	Leu	Ala
	450					455					460				
Gly	Ala	Ile	Val	Val	Glu	Tyr	Ser	Ser	Ser	Val	Lys	Leu	Thr	Ser	Gly
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His	Leu	Lys	Cys	Arg	Leu	Lys	Met	Asp	Lys	Leu	Ala	Leu	Lys	Gly	Thr
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Thr	Tyr	Gly	Met	Cys	Thr	Glu	Lys	Phe	Ser	Phe	Ala	Lys	Asn	Pro	Ala

500					505					510					
Asp	Thr	Gly	His	Gly	Thr	Val	Val	Ile	Glu	Leu	Ser	Tyr	Ser	Gly	Ser
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Asp	Gly	Pro	Cys	Lys	Ile	Pro	Ile	Ala	Ser	Val	Ala	Ser	Leu	Asn	Asp
530					535					540					
Met	Thr	Pro	Val	Gly	Arg	Leu	Val	Thr	Val	Asn	Pro	Phe	Val	Ala	Thr
545					550					555					
Ser	Ser	Ala	Ser	Ser	Lys	Val	Leu	Val	Glu	Met	Glu	Pro	Pro	Phe	Gly
565					570					575					
Asp	Ser	Tyr	Ile	Val	Val	Gly	Arg	Gly	Asp	Lys	Gln	Ile	Asn	His	His
580					585					590					
Trp	His	Lys	Ala	Gly	Ser	Thr	Leu	Gly	Lys	Ala	Phe	Ser	Thr	Thr	Leu
595					600					605					
Lys	Gly	Ala	Gln	Arg	Leu	Ala	Ala	Leu	Gly	Asp	Thr	Ala	Trp	Asp	Phe
610					615					620					
Gly	Ser	Ile	Gly	Gly	Val	Phe	Asn	Ser	Ile	Gly	Lys	Ala	Val	His	Gln
625					630					635					
Val	Phe	Gly	Gly	Ala	Phe	Arg	Thr	Leu	Phe	Gly	Gly	Met	Ser	Trp	Ile
645					650					655					
Thr	Gln	Gly	Leu	Met	Gly	Ala	Leu	Leu	Leu	Trp	Met	Gly	Val	Asn	Ala
660					665					670					
Arg	Asp	Arg	Ser	Ile	Ala	Leu	Ala	Phe	Leu	Ala	Thr	Gly	Gly	Val	Leu
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<210> 19

<211> 5283

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> CDS

<222> (910)...(2965)

<400> 19

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gccgccgcc	atg ggc aag	agg tcc gcc	ggc tca atc	atg tgg ctc	gcg agc	951
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Arg Glu Gly Tyr Met Val Met Arg Ala Ser Gly Arg Asp Ala Ala Ser	
35 40 45	
cag gtc agg gta caa aac gga acg tgc gtc atc ctg gca aca gac atg	1095
Gln Val Arg Val Gln Asn Gly Thr Cys Val Ile Leu Ala Thr Asp Met	
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Gly Glu Trp Cys Glu Asp Ser Ile Thr Tyr Ser Cys Val Thr Ile Asp	
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Gln Glu Glu Glu Pro Val Asp Val Asp Cys Phe Cys Arg Gly Val Asp	
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Arg Val Lys Leu Glu Tyr Gly Arg Cys Gly Arg Gln Ala Gly Ser Arg	
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Gly Arg Gly His Ala Trp Leu Lys Gly Asp Asn Ile Arg Asp His Val	
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acc cga gtc gag ggc tgg atg tgg aag aac aag ctt cta act gcc gcc	1383
Thr Arg Val Glu Gly Trp Met Trp Lys Asn Lys Leu Leu Thr Ala Ala	
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Ile Val Ala Leu Ala Trp Leu Met Val Asp Ser Trp Met Ala Arg Val	
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Cys Thr His Leu Glu Asn Arg Asp Phe Val Thr Gly Thr Gln Gly Thr	
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Thr Arg Val Ser Leu Val Leu Glu Leu Gly Gly Cys Val Thr Ile Thr	
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Ala Glu Gly Lys Pro Ser Ile Asp Val Trp Leu Glu Asp Ile Phe Gln	
225 230 235	

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Asn Thr Lys Val Glu Ala Arg Cys Pro Thr Thr Gly Pro Ala Thr Leu	
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Pro Glu Glu His Gln Ala Asn Met Val Cys Lys Arg Asp Gln Ser Asp	
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Ala Gln Phe Thr Val Ala Ser Glu Lys Val Ile Leu Arg Leu Gly Asp	
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tat gga gat gtg tcg ctg acg tgt aaa gtg gca agt ggg att gat gtc	2055
Tyr Gly Asp Val Ser Leu Thr Cys Lys Val Ala Ser Gly Ile Asp Val	
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gcc caa act gtg gtg atg tca ctc gac agc agc aag gac cac ctg cct	2103
Ala Gln Thr Val Val Met Ser Leu Asp Ser Ser Lys Asp His Leu Pro	
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Ser Ala Trp Gln Val His Arg Asp Trp Phe Glu Asp Leu Ala Leu Pro	
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Trp Lys His Lys Asp Asn Gln Asp Trp Asn Ser Val Glu Lys Leu Val	
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Asp Gln Thr Ala Val Leu Leu Lys Ser Leu Ala Gly Val Pro Leu Ala	
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Cys	Asp	Lys	Ala	Lys	Phe	Lys	Trp	Lys	Arg	Val	Pro	Val	Asp	Ser	Gly	
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<211> 681

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<400> 20

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Trp Leu Leu Leu Asn Val Thr Ser Glu Asp Leu Gly Lys Thr Phe Ser
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Glu	Pro	Asp	Asp	Ile	Asp	Cys	Trp	Cys	Tyr	Gly	Val	Glu	Asn	Val	Arg
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Val	Ala	Tyr	Gly	Lys	Cys	Asp	Ser	Ala	Gly	Arg	Ser	Arg	Arg	Ser	Arg
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Arg	Ala	Ile	Asp	Leu	Pro	Thr	His	Glu	Asn	His	Gly	Leu	Lys	Thr	Arg
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Thr	Ile	Ala	Tyr	Leu	Val	Gly	Ser	Asn	Met	Thr	Gln	Arg	Val	Val	Ile
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Gly	Ile	Thr	Asp	Arg	Asp	Phe	Ile	Glu	Gly	Val	His	Gly	Gly	Thr	Trp
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Val	Ser	Ala	Thr	Leu	Glu	Gln	Asp	Lys	Cys	Val	Thr	Val	Met	Ala	Pro
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Asp	Lys	Pro	Ser	Leu	Asp	Ile	Ser	Leu	Glu	Thr	Val	Ala	Ile	Asp	Arg
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Pro	Ala	Glu	Val	Arg	Lys	Val	Cys	Tyr	Asn	Ala	Val	Leu	Thr	His	Val
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Lys	Ile	Asn	Asp	Lys	Cys	Pro	Ser	Thr	Gly	Glu	Ala	His	Leu	Ala	Glu
			260					265					270		
Glu	Asn	Glu	Gly	Asp	Asn	Ala	Cys	Lys	Arg	Thr	Tyr	Ser	Asp	Arg	Gly
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Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly	Ser	Ile	Val	Ala	Cys
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Thr	Lys	Ile	Gln	Tyr	Val	Ile	Arg	Ala	Gln	Leu	His	Val	Gly	Ala	Lys
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Gln	Glu	Asn	Trp	Thr	Thr	Asp	Ile	Lys	Thr	Leu	Lys	Phe	Asp	Ala	Leu
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Glu	Met	Glu	Thr	Glu	Ser	Trp	Ile	Val	Asp	Arg	Gln	Trp	Ala	Gln	Asp
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Leu	Thr	Leu	Pro	Trp	Gln	Ser	Gly	Ser	Gly	Gly	Val	Trp	Arg	Glu	Met
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His	His	Leu	Val	Glu	Phe	Glu	Pro	Pro	His	Ala	Ala	Thr	Ile	Arg	Val
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Leu	Ala	Leu	Gly	Asn	Gln	Glu	Gly	Ser	Leu	Lys	Thr	Ala	Leu	Thr	Gly
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Ala	Met	Arg	Val	Thr	Lys	Asp	Thr	Asn	Asp	Asn	Asn	Leu	Tyr	Lys	Leu
	450					455				460					
His	Gly	Gly	His	Val	Ser	Cys	Arg	Val	Lys	Leu	Ser	Ala	Leu	Thr	Leu
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Lys	Gly	Thr	Ser	Tyr	Lys	Ile	Cys	Thr	Asp	Lys	Met	Phe	Phe	Val	Lys
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Asn	Pro	Thr	Asp	Thr	Gly	His	Gly	Thr	Val	Val	Met	Gln	Val	Lys	Val
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Ser	Lys	Gly	Ala	Pro	Cys	Arg	Ile	Pro	Val	Ile	Val	Ala	Asp	Asp	Leu
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Thr	Ala	Ala	Ile	Asn	Lys	Gly	Ile	Leu	Val	Thr	Val	Asn	Pro	Ile	Ala
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Ser	Thr	Asn	Asp	Asp	Glu	Val	Leu	Ile	Glu	Val	Asn	Pro	Pro	Phe	Gly
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Asp	Ser	Tyr	Ile	Ile	Val	Gly	Arg	Gly	Asp	Ser	Arg	Leu	Thr	Tyr	Gln
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Lys	Gly	Val	Glu	Arg	Leu	Ala	Val	Met	Gly	Asp	Thr	Ala	Trp	Asp	Phe
		595					600					605			
Ser	Ser	Ala	Gly	Gly	Phe	Phe	Thr	Ser	Val	Gly	Lys	Gly	Ile	His	Thr
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 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note =
 synthetic construct

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 <222> (910)...(2986)

<400> 21

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Gln Gly Lys Val Leu Met Ser Ile Asn Lys Thr Asp Ala Gln Ser Ala			
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Leu Asp Val Gly Val Met Cys Lys Asp Asp Ile Thr Tyr Leu Cys Pro			
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Ser Phe Asn Cys Leu Gly Thr Ser Asn Arg Asp Phe Val Glu Gly Ala			
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agt ggg gca aca tgg att gac ttg gta ctt gaa ggg gga agc tgt gtc			1575
Ser Gly Ala Thr Trp Ile Asp Leu Val Leu Glu Gly Gly Ser Cys Val			
	210	215	220
aca gtg atg gca cca gag aaa cca aca ctg gac ttc aaa gtg atg aag			1623
Thr Val Met Ala Pro Glu Lys Pro Thr Leu Asp Phe Lys Val Met Lys			
	225	230	235

atg gag gct acc gag tta gcc act gtg cgt gag tat tgt tac gaa gca	1671
Met Glu Ala Thr Glu Leu Ala Thr Val Arg Glu Tyr Cys Tyr Glu Ala	
240 245 250	
acc ttg gac acg ctg tca aca gtg gca agg tgc ccc aca aca gga gaa	1719
Thr Leu Asp Thr Leu Ser Thr Val Ala Arg Cys Pro Thr Thr Gly Glu	
255 260 265 270	
gct cac aac acc aaa agg agt gac cca aca ttt gtc tgc aaa aga gat	1767
Ala His Asn Thr Lys Arg Ser Asp Pro Thr Phe Val Cys Lys Arg Asp	
275 280 285	
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Val Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly	
290 295 300	
agc att gac aca tgc gct aag ttc aca tgc aaa aac aag gca aca ggg	1863
Ser Ile Asp Thr Cys Ala Lys Phe Thr Cys Lys Asn Lys Ala Thr Gly	
305 310 315	
aag acg atc ttg aga gaa aac atc aag tat gag gtt gca atc ttt gtg	1911
Lys Thr Ile Leu Arg Glu Asn Ile Lys Tyr Glu Val Ala Ile Phe Val	
320 325 330	
cat ggt tca acg gac tct acg tca cat ggc aat tac tct gag cag att	1959
His Gly Ser Thr Asp Ser Thr Ser His Gly Asn Tyr Ser Glu Gln Ile	
335 340 345 350	
gga aaa aac caa gcg gct aga ttc acc ata agc ccg caa gca ccg tcc	2007
Gly Lys Asn Gln Ala Ala Arg Phe Thr Ile Ser Pro Gln Ala Pro Ser	
355 360 365	
ttt acg gcc aac atg ggc gag tat gga aca gtt acc att gat tgt gaa	2055
Phe Thr Ala Asn Met Gly Glu Tyr Gly Thr Val Thr Ile Asp Cys Glu	
370 375 380	
gca aga tca gga atc aac acg gag gat tat tat gtt ttc act gtc aag	2103
Ala Arg Ser Gly Ile Asn Thr Glu Asp Tyr Tyr Val Phe Thr Val Lys	
385 390 395	
gag aag tca tgg cta gtg aac agg gac tgg ttt cac gac ttg aac ctt	2151
Glu Lys Ser Trp Leu Val Asn Arg Asp Trp Phe His Asp Leu Asn Leu	
400 405 410	
cca tgg acg agc cct gcc aca act gat tgg cgc aac aga gaa aca ctg	2199
Pro Trp Thr Ser Pro Ala Thr Thr Asp Trp Arg Asn Arg Glu Thr Leu	
415 420 425 430	
gtg gaa ttt gag gaa ccg cat gcc acc aag caa act gta gta gcc cta	2247
Val Glu Phe Glu Glu Pro His Ala Thr Lys Gln Thr Val Val Ala Leu	
435 440 445	
gga tcg caa gaa ggt gcc ctg cac aca gca ttg gct gga gcc att cca	2295
Gly Ser Gln Glu Gly Ala Leu His Thr Ala Leu Ala Gly Ala Ile Pro	

450										455										460										
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Ala	Thr	Val	Ser	Ser	Ser	Thr	Leu	Thr	Leu	Gln	Ser	Gly	His	Leu	Lys															
		465						470				475																		
tgc	aga	gct	aag	ctt	gac	aag	gtc	aaa	atc	aag	gga	acg	aca	tat	ggc		2391													
Cys	Arg	Ala	Lys	Leu	Asp	Lys	Val	Lys	Ile	Lys	Gly	Thr	Thr	Tyr	Gly															
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Met	Cys	Asp	Ser	Ala	Phe	Thr	Phe	Ser	Lys	Asn	Pro	Thr	Asp	Thr	Gly															
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cac	ggg	aca	gtg	att	gtg	gaa	ctg	cag	tat	act	gga	agc	aac	gga	ccc		2487													
His	Gly	Thr	Val	Ile	Val	Glu	Leu	Gln	Tyr	Thr	Gly	Ser	Asn	Gly	Pro															
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tgc	cga	gtt	ccc	atc	tcc	gtg	act	gca	aac	ctc	atg	gat	ttg	aca	ccg		2535													
Cys	Arg	Val	Pro	Ile	Ser	Val	Thr	Ala	Asn	Leu	Met	Asp	Leu	Thr	Pro															
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gtt	gga	aga	ttg	gtc	acg	gtc	aat	ccc	ttt	ata	agc	aca	ggg	gga	gcg		2583													
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aac	aac	aag	gtc	atg	atc	gaa	gtt	gaa	cca	ccc	ttt	ggc	gat	tct	tac		2631													
Asn	Asn	Lys	Val	Met	Ile	Glu	Val	Glu	Pro	Pro	Phe	Gly	Asp	Ser	Tyr															
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atc	gtc	gtc	gga	aga	ggc	acc	acc	cag	att	aac	tac	cac	tgg	cac	aaa		2679													
Ile	Val	Val	Gly	Arg	Gly	Thr	Thr	Gln	Ile	Asn	Tyr	His	Trp	His	Lys															
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Glu	Gly	Ser	Ser	Ile	Gly	Lys	Ala	Leu	Ala	Thr	Thr	Trp	Lys	Gly	Ala															
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caa	cgg	cta	gcc	gtc	tta	ggg	gac	aca	gcg	tgg	gac	ttt	gga	tct	att		2775													
Gln	Arg	Leu	Ala	Val	Leu	Gly	Asp	Thr	Ala	Trp	Asp	Phe	Gly	Ser	Ile															
			610					615					620																	
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		625					630					635																		
gga	gcg	ttc	agg	act	ctg	ttc	ggg	gga	atg	tcc	tgg	atc	aca	cag	ggg		2871													
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655					660					665					670															
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Ser Ile Ser Leu Thr Leu Leu Ala Val Gly Gly Ile Leu Ile Phe Leu
675 680 685

gca acc agc gtg caa gcc t gagcggccgc tcgagcatgc atctagaggg 3016
Ala Thr Ser Val Gln Ala
690

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<210> 22

<211> 692

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

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			20					25					30		
Lys	Val	Leu	Met	Ser	Ile	Asn	Lys	Thr	Asp	Ala	Gln	Ser	Ala	Ile	Asn
		35					40					45			
Ile	Pro	Ser	Ala	Asn	Gly	Ala	Asn	Thr	Cys	Ile	Val	Arg	Ala	Leu	Asp
	50					55					60				
Val	Gly	Val	Met	Cys	Lys	Asp	Asp	Ile	Thr	Tyr	Leu	Cys	Pro	Val	Leu
65					70					75					80
Ser	Ala	Gly	Asn	Asp	Pro	Glu	Asp	Ile	Asp	Cys	Trp	Cys	Asp	Val	Glu
				85					90					95	
Glu	Val	Trp	Val	His	Tyr	Gly	Arg	Cys	Thr	Arg	Met	Gly	His	Ser	Arg
			100					105					110		
Arg	Ser	Arg	Arg	Ser	Ile	Ser	Val	Gln	His	His	Gly	Asp	Ser	Thr	Leu
		115					120					125			
Ala	Thr	Lys	Asn	Thr	Pro	Trp	Leu	Asp	Thr	Val	Lys	Thr	Thr	Lys	Tyr
						135					140				
Leu	Thr	Lys	Val	Glu	Asn	Trp	Val	Leu	Arg	Asn	Pro	Gly	Tyr	Ala	Leu
145					150					155					160
Val	Ala	Leu	Ala	Ile	Gly	Trp	Met	Leu	Gly	Ser	Asn	Asn	Thr	Gln	Arg
				165					170					175	
Val	Val	Phe	Val	Ile	Met	Leu	Met	Leu	Ile	Ala	Pro	Ala	Tyr	Ser	Phe
			180					185					190		
Asn	Cys	Leu	Gly	Thr	Ser	Asn	Arg	Asp	Phe	Val	Glu	Gly	Ala	Ser	Gly
		195					200					205			
Ala	Thr	Trp	Ile	Asp	Leu	Val	Leu	Glu	Gly	Gly	Ser	Cys	Val	Thr	Val
		210				215						220			
Met	Ala	Pro	Glu	Lys	Pro	Thr	Leu	Asp	Phe	Lys	Val	Met	Lys	Met	Glu
225					230					235					240
Ala	Thr	Glu	Leu	Ala	Thr	Val	Arg	Glu	Tyr	Cys	Tyr	Glu	Ala	Thr	Leu
				245					250					255	
Asp	Thr	Leu	Ser	Thr	Val	Ala	Arg	Cys	Pro	Thr	Thr	Gly	Glu	Ala	His
			260					265					270		
Asn	Thr	Lys	Arg	Ser	Asp	Pro	Thr	Phe	Val	Cys	Lys	Arg	Asp	Val	Val
		275					280					285			
Asp	Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly	Ser	Ile
		290				295					300				
Asp	Thr	Cys	Ala	Lys	Phe	Thr	Cys	Lys	Asn	Lys	Ala	Thr	Gly	Lys	Thr
305					310					315					320
Ile	Leu	Arg	Glu	Asn	Ile	Lys	Tyr	Glu	Val	Ala	Ile	Phe	Val	His	Gly
				325					330					335	
Ser	Thr	Asp	Ser	Thr	Ser	His	Gly	Asn	Tyr	Ser	Glu	Gln	Ile	Gly	Lys
			340					345					350		
Asn	Gln	Ala	Ala	Arg	Phe	Thr	Ile	Ser	Pro	Gln	Ala	Pro	Ser	Phe	Thr
		355					360					365			
Ala	Asn	Met	Gly	Glu	Tyr	Gly	Thr	Val	Thr	Ile	Asp	Cys	Glu	Ala	Arg
	370					375					380				
Ser	Gly	Ile	Asn	Thr	Glu	Asp	Tyr	Tyr	Val	Phe	Thr	Val	Lys	Glu	Lys
385					390					395					400
Ser	Trp	Leu	Val	Asn	Arg	Asp	Trp	Phe	His	Asp	Leu	Asn	Leu	Pro	Trp
				405					410					415	
Thr	Ser	Pro	Ala	Thr	Thr	Asp	Trp	Arg	Asn	Arg	Glu	Thr	Leu	Val	Glu
			420					425					430		
Phe	Glu	Glu	Pro	His	Ala	Thr	Lys	Gln	Thr	Val	Val	Ala	Leu	Gly	Ser
		435					440					445			
Gln	Glu	Gly	Ala	Leu	His	Thr	Ala	Leu	Ala	Gly	Ala	Ile	Pro	Ala	Thr

450		455		460	
Val	Ser	Ser	Ser	Thr	Leu
465		470		475	
Ala	Lys	Leu	Asp	Lys	Val
		485		490	
Asp	Ser	Ala	Phe	Thr	Phe
		500		505	
Thr	Val	Ile	Val	Glu	Leu
		515		520	
Val	Pro	Ile	Ser	Val	Thr
		530		535	
Arg	Leu	Val	Thr	Val	Asn
545				550	
Lys	Val	Met	Ile	Glu	Val
				565	
Val	Gly	Arg	Gly	Thr	Thr
				580	
Ser	Ser	Ile	Gly	Lys	Ala
		595		600	
Leu	Ala	Val	Leu	Gly	Asp
610				615	
Val	Phe	Asn	Ser	Ile	Gly
625				630	
Phe	Arg	Thr	Leu	Phe	Gly
				645	
Gly	Ala	Leu	Leu	Trp	Met
		660		665	
Ser	Leu	Thr	Leu	Leu	Ala
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Ser	Val	Gln	Ala		
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<210> 23
 <211> 5271
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of artificial sequence; note =
 synthetic construct

<221> CDS
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gattattgac	tagttattaa
tggagttccg	cgttacataa
cccgccatt	gacgtcaata
attgacgtca	atgggtggac
atcatatgcc	aagtacgccc
atgccagta	catgacctta
tcgctattac	catgggtgatg
actcacgggg	atttccaagt
	ctccacccca
	ttgacgtcaa
	tgggagtttg
	ttttggcacc
	60
	120
	180
	240
	300
	360
	420
	480
	540
	600
	660
	720

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gtaggcgtgt acgggtgggag gtctatataa gcagagctct ctggctaact agagaaccca	840
ctgcttactg gcttatcgaa attaatacga ctcactatag ggagacccaa gcttggtacc	900
gccgccgcc atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc	951
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser	
1 5 10	
ttg gca gtt gtc ata gct ggt aca agc gct gtg acc ttg gtg cgg aaa	999
Leu Ala Val Val Ile Ala Gly Thr Ser Ala Val Thr Leu Val Arg Lys	
15 20 25 30	
aac aga tgg ttg ctc cta aat gtg aca tct gag gac ctc ggg aaa aca	1047
Asn Arg Trp Leu Leu Leu Asn Val Thr Ser Glu Asp Leu Gly Lys Thr	
35 40 45	
ttc tct gtg ggc aca ggc aac tgc aca aca aac att ttg gaa gcc aag	1095
Phe Ser Val Gly Thr Gly Asn Cys Thr Thr Asn Ile Leu Glu Ala Lys	
50 55 60	
tac tgg tgc cca gac tca atg gaa tac aac tgt ccc aat ctc agt cca	1143
Tyr Trp Cys Pro Asp Ser Met Glu Tyr Asn Cys Pro Asn Leu Ser Pro	
65 70 75	
aga gag gag cca gat gac att gat tgc tgg tgc tat ggg gtg gaa aac	1191
Arg Glu Glu Pro Asp Asp Ile Asp Cys Trp Cys Tyr Gly Val Glu Asn	
80 85 90	
gtt aga gtc gca tat ggt aag tgt gac tca gca ggc agg tct agg agg	1239
Val Arg Val Ala Tyr Gly Lys Cys Asp Ser Ala Gly Arg Ser Arg Arg	
95 100 105 110	
tca aga agg gcc att gac ttg cct acg cat gaa aac cat ggt ttg aag	1287
Ser Arg Arg Ala Ile Asp Leu Pro Thr His Glu Asn His Gly Leu Lys	
115 120 125	
acc cgg caa gaa aaa tgg atg act gga aga atg ggt gaa agg caa ctc	1335
Thr Arg Gln Glu Lys Trp Met Thr Gly Arg Met Gly Glu Arg Gln Leu	
130 135 140	
caa aag att gag aga tgg ttc gtg agg aac ccc ttt ttt gca gtg acg	1383
Gln Lys Ile Glu Arg Trp Phe Val Arg Asn Pro Phe Phe Ala Val Thr	
145 150 155	
gct ctg acc att gcc tac ctt gtg gga agc aac atg acg caa cga gtc	1431
Ala Leu Thr Ile Ala Tyr Leu Val Gly Ser Asn Met Thr Gln Arg Val	
160 165 170	
gtg att gcc cta ctg gtc ttg gct gtt ggt ccg gcc tac tca gct cac	1479
Val Ile Ala Leu Leu Val Leu Ala Val Gly Pro Ala Tyr Ser Ala His	
175 180 185 190	
tgc att gga att act gac agg gat ttc att gag ggg gtg cat gga gga	1527
Cys Ile Gly Ile Thr Asp Arg Asp Phe Ile Glu Gly Val His Gly Gly	
195 200 205	

act tgg gtt tca gct acc ctg gag caa gac aag tgt gtc act gtt atg	1575
Thr Trp Val Ser Ala Thr Leu Glu Gln Asp Lys Cys Val Thr Val Met	
210 215 220	
gcc cct gac aag cct tca ttg gac atc tca cta gag aca gta gcc att	1623
Ala Pro Asp Lys Pro Ser Leu Asp Ile Ser Leu Glu Thr Val Ala Ile	
225 230 235	
gat aga cct gct gag gtg agg aaa gtg tgt tac aat gca gtt ctc act	1671
Asp Arg Pro Ala Glu Val Arg Lys Val Cys Tyr Asn Ala Val Leu Thr	
240 245 250	
cat gtg aag att aat gac aag tgc ccc agc act gga gag gcc cac cta	1719
His Val Lys Ile Asn Asp Lys Cys Pro Ser Thr Gly Glu Ala His Leu	
255 260 265 270	
gct gaa gag aac gaa ggg gac aat gcg tgc aag cgc act tat tct gat	1767
Ala Glu Glu Asn Glu Gly Asp Asn Ala Cys Lys Arg Thr Tyr Ser Asp	
275 280 285	
aga ggc tgg ggc aat ggc tgt ggc cta ttt ggg aaa ggg agc att gtg	1815
Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser Ile Val	
290 295 300	
gca tgc gcc aaa ttc act tgt gcc aaa tcc atg agt ttg ttt gag gtt	1863
Ala Cys Ala Lys Phe Thr Cys Ala Lys Ser Met Ser Leu Phe Glu Val	
305 310 315	
gat cag acc aaa att cag tat gtc atc aga gca caa ttg cat gta ggg	1911
Asp Gln Thr Lys Ile Gln Tyr Val Ile Arg Ala Gln Leu His Val Gly	
320 325 330	
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Ala Lys Gln Glu Asn Trp Thr Thr Asp Ile Lys Thr Leu Lys Phe Asp	
335 340 345 350	
gcc ctg tca ggc tcc cag gaa gtc gag ttc att ggg tat gga aaa gct	2007
Ala Leu Ser Gly Ser Gln Glu Val Glu Phe Ile Gly Tyr Gly Lys Ala	
355 360 365	
aca ctg gaa tgc cag gtg caa act gcg gtg gac ttt ggt aac agt tac	2055
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370 375 380	
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Ile Ala Glu Met Glu Thr Glu Ser Trp Ile Val Asp Arg Gln Trp Ala	
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Gln Asp Leu Thr Leu Pro Trp Gln Ser Gly Ser Gly Gly Val Trp Arg	
400 405 410	
gag atg cat cat ctt gtc gaa ttt gaa cct ccg cat gcc gcc act atc	2199
Glu Met His His Leu Val Glu Phe Glu Pro Pro His Ala Ala Thr Ile	
415 420 425 430	

aga gta ctg gcc ctg gga aac cag gaa ggc tcc ttg aaa aca gct ctt	2247
Arg Val Leu Ala Leu Gly Asn Gln Glu Gly Ser Leu Lys Thr Ala Leu	
435 440 445	
act ggc gca atg agg gtt aca aag gac aca aat gac aac aac ctt tac	2295
Thr Gly Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Asn Leu Tyr	
450 455 460	
aaa cta cat ggt gga cat gtt tct tgc aga gtg aaa ttg tca gct ttg	2343
Lys Leu His Gly Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu	
465 470 475	
aca ctc aag ggg aca tcc tac aaa ata tgc act gac aaa atg ttt ttt	2391
Thr Leu Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe	
480 485 490	
gtc aag aac cca act gac act ggc cat ggc act gtt gtg atg cag gtg	2439
Val Lys Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val	
495 500 505 510	
aaa gtg tca aaa gga gcc ccc tgc agg att cca gtg ata gta gct gat	2487
Lys Val Ser Lys Gly Ala Pro Cys Arg Ile Pro Val Ile Val Ala Asp	
515 520 525	
gat ctt aca gcg gca atc aat aaa ggc att ttg gtt aca gtt aac ccc	2535
Asp Leu Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro	
530 535 540	
atc gcc tca acc aat gat gat gaa gtg ctg att gag gtg aac cca cct	2583
Ile Ala Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro	
545 550 555	
ttt gga gac agc tac att atc gtt ggg aga gga gat tca cgt ctc act	2631
Phe Gly Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr	
560 565 570	
tac cag tgg cac aaa gag gga agc tca ata gga aag ttg ttc act cag	2679
Tyr Gln Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln	
575 580 585 590	
acc atg aaa ggc gtg gaa cgc ctg gcc gtc atg gga gac acc gcc tgg	2727
Thr Met Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp	
595 600 605	
gat ttc agc tcc gct gga ggg ttc ttc act tcg gtt ggg aaa gga att	2775
Asp Phe Ser Ser Ala Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile	
610 615 620	
cat acg gtg ttt ggc tct gcc ttt cag ggg cta ttt ggc ggc ttg aac	2823
His Thr Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn	
625 630 635	
tgg ata aca aag gtc atc atg ggg gcg gta ctt ata tgg gtt ggc atc	2871
Trp Ile Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile	

640	645	650	
aac aca aga aac atg aca atg tcc atg agc atg		atc ttg gta gga gtg	2919
Asn Thr Arg Asn Met Thr Met Ser Met Ser Met		Ile Leu Val Gly Val	
655	660	665	670
atc atg atg ttt ttg tct cta gga gtt ggg gcg t gagcggccgc			2963
Ile Met Met Phe Leu Ser Leu Gly Val Gly Ala			
	675	680	
tcgagcatgc atctagaggg ccctattcta tagtgtcacc taaatgctag agctcgctga			3023
tcagcctcga ctgtgccttc tagttgccag ccatctgttg tttgcccctc ccccgctgct			3083
tccttgaccc tggaaggtgc cactcccaact gtcctttcct aataaaatga ggaaattgca			3143
tcgcattgtc tgagtaggtg tcattctatt ctgggggggtg ggggtggggca ggacagcaag			3203
ggggaggatt gggaagacaa tagcaggcat gctggggatg cgggtgggctc tatggcttct			3263
gaggcgga aaacagctgc attaatgaat cggccaacgc gcggggagag gcggtttgcg			3323
tattgggcgc tcttcgcgtt cctcgctcac tgactcgctg cgctcggtcg ttcggctgcg			3383
gcgagcggta tcagctcact caaaggcggg aatacggtta tccacagaat caggggataa			3443
cgcaggaaaag aacatgtgag caaaaggcca gcaaaaggcc aggaaccgta aaaaggccgc			3503
gttgctggcg tttttccata ggctccgccc ccctgacgag catcacaaaa atcgacgctc			3563
aagtcagagg tggcgaacc cgacaggact ataaagatac caggcgtttc cccctggaag			3623
ctccctcggt cgctctctg ttcgcacct gccgcttacc ggatacctgt ccgcctttct			3683
cccttcggga agcgtggcgc tttctcaatg ctacgctgt aggtatctca gttcgggtga			3743
ggtcgttcgc tccaagctgg gctgtgtgca cgaaccccc gttcagccc accgctgcgc			3803
cttatccggt aactatcgtc ttgagtc aaaccccc cagcacttat cgccactggc			3863
agcagccact ggtaacagga ttagcagagc gaggtatgta ggcggtgcta cagagttctt			3923
gaagtgggtg cctaactacg gctacactag aaggacagta tttggtatct gcgctctgct			3983
gaagccagtt accttcgga aaagagttgg tagctcttga tccggcaaac aaaccacgc			4043
tggtagcggg ggtttttttg tttgcaagca gcagattacg cgcagaaaaa aaggatctca			4103
agaagatcct ttgatcttt ctacgggggtc tgacgctcag tggaacgaaa actcacgtta			4163
agggattttg gtcatgagat tatcaaaaag gatcttcacc tagatccttt taaattaaaa			4223
atgaagtttt aaatcaatct aaagtatata tgagtaaact tgggtctgaca gttaccaatg			4283
cttaatcagt gaggcaccta tctcagcgat ctgtctattt cgttcatcca tagttgcctg			4343
actccccgtc gtgtagataa ctacgatac ggagggctta ccatctggcc ccagtgtgc			4403
aatgataccg cgagaccac gctcaccggc tccagattta tcagcaataa accagccagc			4463
cggaagggcc gagcgcagaa gtggtcctgc aactttatcc gcctccatcc agtctattaa			4523
ttgttgccgg gaagctagag taagtgttc gccagttaat agtttgcgca acgttgttg			4583
cattgctaca ggcacgtgg tgtcacgctc gtcgtttggg atggcttcat tcagctccgg			4643
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ggcagcactg cataattctc ttactgtcat gccatccgta agatgcttt ctgtgactgg			4823
tgagtactca accaagtcac tctgagaata gtgtatgcgg cgaccgagtt gctcttgccc			4883
ggcgtaataa cgggataata ccgcgccaca tagcagaact ttaaaagtgc tcatcattgg			4943
aaaacgttct tcggggcgaa aactctcaag gatcttaccg ctggttgagat ccagttcgat			5003
gtaaccact cgtgcaccca actgatcttc agcatctttt actttcacca gcgtttctgg			5063
gtgagcaaaa acaggaaggc aaaatgccgc aaaaaaggga ataaggcgca cacggaaatg			5123
ttgaatactc atactcttcc tttttcaata ttattgaagc atttatcagg gttattgtct			5183
catgagcgga tacatatttg aatgtattta gaaaaataaa caaatagggg ttccgcgcac			5243
atttccccga aaagtgccac ctgacgtc			5271

<210> 24

<211> 681

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =

synthetic construct

<400> 24

Met	Gly	Lys	Arg	Ser	Ala	Gly	Ser	Ile	Met	Trp	Leu	Ala	Ser	Leu	Ala
1				5					10					15	
Val	Val	Ile	Ala	Gly	Thr	Ser	Ala	Val	Thr	Leu	Val	Arg	Lys	Asn	Arg
			20					25					30		
Trp	Leu	Leu	Leu	Asn	Val	Thr	Ser	Glu	Asp	Leu	Gly	Lys	Thr	Phe	Ser
		35					40					45			
Val	Gly	Thr	Gly	Asn	Cys	Thr	Thr	Asn	Ile	Leu	Glu	Ala	Lys	Tyr	Trp
	50					55					60				
Cys	Pro	Asp	Ser	Met	Glu	Tyr	Asn	Cys	Pro	Asn	Leu	Ser	Pro	Arg	Glu
65				70					75					80	
Glu	Pro	Asp	Asp	Ile	Asp	Cys	Trp	Cys	Tyr	Gly	Val	Glu	Asn	Val	Arg
				85				90						95	
Val	Ala	Tyr	Gly	Lys	Cys	Asp	Ser	Ala	Gly	Arg	Ser	Arg	Arg	Ser	Arg
			100					105					110		
Arg	Ala	Ile	Asp	Leu	Pro	Thr	His	Glu	Asn	His	Gly	Leu	Lys	Thr	Arg
	115						120					125			
Gln	Glu	Lys	Trp	Met	Thr	Gly	Arg	Met	Gly	Glu	Arg	Gln	Leu	Gln	Lys
	130					135					140				
Ile	Glu	Arg	Trp	Phe	Val	Arg	Asn	Pro	Phe	Phe	Ala	Val	Thr	Ala	Leu
145					150				155						160
Thr	Ile	Ala	Tyr	Leu	Val	Gly	Ser	Asn	Met	Thr	Gln	Arg	Val	Val	Ile
				165				170						175	
Ala	Leu	Leu	Val	Leu	Ala	Val	Gly	Pro	Ala	Tyr	Ser	Ala	His	Cys	Ile
			180					185					190		
Gly	Ile	Thr	Asp	Arg	Asp	Phe	Ile	Glu	Gly	Val	His	Gly	Gly	Thr	Trp
	195					200						205			
Val	Ser	Ala	Thr	Leu	Glu	Gln	Asp	Lys	Cys	Val	Thr	Val	Met	Ala	Pro
	210					215					220				
Asp	Lys	Pro	Ser	Leu	Asp	Ile	Ser	Leu	Glu	Thr	Val	Ala	Ile	Asp	Arg
225				230					235					240	
Pro	Ala	Glu	Val	Arg	Lys	Val	Cys	Tyr	Asn	Ala	Val	Leu	Thr	His	Val
				245				250						255	
Lys	Ile	Asn	Asp	Lys	Cys	Pro	Ser	Thr	Gly	Glu	Ala	His	Leu	Ala	Glu
		260						265					270		
Glu	Asn	Glu	Gly	Asp	Asn	Ala	Cys	Lys	Arg	Thr	Tyr	Ser	Asp	Arg	Gly
	275					280						285			
Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly	Ser	Ile	Val	Ala	Cys
	290				295						300				
Ala	Lys	Phe	Thr	Cys	Ala	Lys	Ser	Met	Ser	Leu	Phe	Glu	Val	Asp	Gln
305				310					315					320	
Thr	Lys	Ile	Gln	Tyr	Val	Ile	Arg	Ala	Gln	Leu	His	Val	Gly	Ala	Lys
			325					330						335	
Gln	Glu	Asn	Trp	Thr	Thr	Asp	Ile	Lys	Thr	Leu	Lys	Phe	Asp	Ala	Leu
		340					345						350		
Ser	Gly	Ser	Gln	Glu	Val	Glu	Phe	Ile	Gly	Tyr	Gly	Lys	Ala	Thr	Leu
	355					360						365			
Glu	Cys	Gln	Val	Gln	Thr	Ala	Val	Asp	Phe	Gly	Asn	Ser	Tyr	Ile	Ala
	370					375					380				
Glu	Met	Glu	Thr	Glu	Ser	Trp	Ile	Val	Asp	Arg	Gln	Trp	Ala	Gln	Asp
385				390					395					400	
Leu	Thr	Leu	Pro	Trp	Gln	Ser	Gly	Ser	Gly	Gly	Val	Trp	Arg	Glu	Met
			405					410						415	
His	His	Leu	Val	Glu	Phe	Glu	Pro	Pro	His	Ala	Ala	Thr	Ile	Arg	Val
			420					425						430	

Leu Ala Leu Gly Asn Gln Glu Gly Ser Leu Lys Thr Ala Leu Thr Gly
 435 440 445
 Ala Met Arg Val Thr Lys Asp Thr Asn Asp Asn Asn Leu Tyr Lys Leu
 450 455 460
 His Gly Gly His Val Ser Cys Arg Val Lys Leu Ser Ala Leu Thr Leu
 465 470 475 480
 Lys Gly Thr Ser Tyr Lys Ile Cys Thr Asp Lys Met Phe Phe Val Lys
 485 490 495
 Asn Pro Thr Asp Thr Gly His Gly Thr Val Val Met Gln Val Lys Val
 500 505 510
 Ser Lys Gly Ala Pro Cys Arg Ile Pro Val Ile Val Ala Asp Asp Leu
 515 520 525
 Thr Ala Ala Ile Asn Lys Gly Ile Leu Val Thr Val Asn Pro Ile Ala
 530 535 540
 Ser Thr Asn Asp Asp Glu Val Leu Ile Glu Val Asn Pro Pro Phe Gly
 545 550 555 560
 Asp Ser Tyr Ile Ile Val Gly Arg Gly Asp Ser Arg Leu Thr Tyr Gln
 565 570 575
 Trp His Lys Glu Gly Ser Ser Ile Gly Lys Leu Phe Thr Gln Thr Met
 580 585 590
 Lys Gly Val Glu Arg Leu Ala Val Met Gly Asp Thr Ala Trp Asp Phe
 595 600 605
 Ser Ser Ala Gly Gly Phe Phe Thr Ser Val Gly Lys Gly Ile His Thr
 610 615 620
 Val Phe Gly Ser Ala Phe Gln Gly Leu Phe Gly Gly Leu Asn Trp Ile
 625 630 635 640
 Thr Lys Val Ile Met Gly Ala Val Leu Ile Trp Val Gly Ile Asn Thr
 645 650 655
 Arg Asn Met Thr Met Ser Met Ser Met Ile Leu Val Gly Val Ile Met
 660 665 670
 Met Phe Leu Ser Leu Gly Val Gly Ala
 675 680

<210> 25

<211> 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature

<222> 1-35

<223> POW 454

<400> 25

aaaagaaaaa gcgctaccac catccaccgg gacag

35

<210> 26

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature

<222> 1-41

<223> CPOW 2417

<400> 26

actgttacc tcaaccccggt actcgccggc gaaaaagaaa a

41

<210> 27

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<223> Modified JE Signal

<400> 27

Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala

1 5 10 15

Val Val Ile Ala Gly Thr Ser Ala

20

<210> 28

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature

<222> 1-36

<223> YF 482

<400> 28

aaaagaaaaa gcgctgtgac cttggtgcgg aaaaac

36

<210> 29

<211> 41

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature

<222> 1-41

<223> CYF 2433

<400> 29

acagagatcc tcaaccccggt actcgccggc gaaaaagaaa a

41

<210> 30
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature
<222> 1-41
<223> SLE 463

<400> 30
aaaagaaaaa gcgctttgca gttatcaacc tatcagggga a

41

<210> 31
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<221> misc_feature
<222> 1-40
<223> CSLE 2477

<400> 31
accgttggtc gcacgttcgg actcgccggc gaaaaagaaa

40

<210> 32
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<400> 32
Leu Asp Thr Ile Asn Arg Arg Pro Ser Lys Lys Arg Gly Gly Thr Arg
1 5 10 15
Ser Leu Leu Gly Leu Ala Ala Leu Ile Gly Leu Ala Ser Ser Leu Gln
20 25 30
Leu Leu Ser Thr Tyr Gln Gly
35

<210> 33
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<400> 33
Met Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Met
1 5 10 15
Lys Leu Ser Asn Phe Gln Gly Lys
20

<210> 34
<211> 30
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<400> 34
Met Asn Glu Gly Ser Ile Met Trp Leu Ala Ser Leu Ala Val Val Ile
1 5 10 15
Ala Cys Ala Gly Ala Met Lys Leu Ser Asn Phe Gln Gly Lys
20 25 30

<210> 35
<211> 39
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<400> 35
Met Gly Arg Lys Gln Asn Lys Arg Gly Gly Asn Glu Gly Ser Ile Met
1 5 10 15
Trp Leu Ala Ser Leu Ala Val Val Ile Ala Cys Ala Gly Ala Met Lys
20 25 30
Leu Ser Asn Phe Gln Gly Lys
35

<210> 36
<211> 34
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<400> 36
Met Ser Lys Lys Arg Gly Gly Ser Glu Thr Ser Val Leu Met Val Ile
1 5 10 15
Phe Met Leu Ile Gly Phe Ala Ala Ala Leu Lys Leu Ser Asn Phe Gln
20 25 30
Gly Lys

<210> 37

<211> 33
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<400> 37
Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser Leu Ala
1 5 10 15
Val Val Ile Ala Cys Ala Gly Ala Val Thr Leu Ser Asn Phe Gln Gly
20 25 30
Lys

<210> 38
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<400> 38
Met Asn Val Leu Arg Gly Phe Arg Lys Glu Ile Gly Arg Met Leu Asn
1 5 10 15
Ile Leu Asn Arg Arg Arg Arg Thr Ala Gly Met Ile Ile Met Leu Ile
20 25 30
Pro Thr Val Met Ala Phe His Leu Thr Thr Arg Asn Gly Glu
35 40 45

<210> 39
<211> 40
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<400> 39
Met Val Gly Leu Gln Lys Arg Gly Lys Arg Arg Ser Ala Thr Asp Trp
1 5 10 15
Met Ser Trp Leu Leu Val Ile Thr Leu Leu Gly Met Thr Leu Ala Ala
20 25 30
Thr Val Arg Lys Glu Arg Gly Asp
35 40

<210> 40
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =

synthetic construct

<400> 40

Met Gly Trp Leu Leu Val Val Val Leu Leu Gly Val Thr Leu Ala Ala
 1 5 10 15
 Thr Val Arg Lys Glu Arg Gly Asp
 20

<210> 41

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
 synthetic construct

<400> 41

Met Ser Trp Leu Leu Val Ile Thr Leu Leu Gly Met Thr Ile Ala Ala
 1 5 10 15
 Thr Val Arg Lys Glu Arg Gly Asp
 20

<210> 42

<211> 5292

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
 synthetic construct

<221> CDS

<222> (910)...(2964)

<400> 42

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ccgcatagtt	aagccagtat	ctgctccctg	cttgtgtgtt	ggaggtcgct	gagtagtgcg	120
cgagcaaaat	ttaagctaca	acaaggcaag	gcttgaccga	caattgcatg	aagaatctgc	180
ttagggttag	gcgttttgcg	ctgcttcgcg	atgtacgggc	cagatatacg	cgttgacatt	240
gattattgac	tagttattaa	tagtaatcaa	ttacggggtc	attagttcat	agcccatata	300
tggagttccg	cgttacataa	cttacggtaa	atggcccgcg	tggctgaccg	cccaacgacc	360
cccgccatt	gacgtcaata	atgacgtatg	ttcccatagt	aacgccaata	gggactttcc	420
attgacgtca	atgggtggag	tatttacggt	aaactgcccc	cttggcagta	catcaagtgt	480
atcatatgcc	aagtacgccc	cctattgacg	tcaatgacgg	taaatggccc	gcctggcatt	540
atgcccagta	catgacctta	tgggactttc	ctacttgcca	gtacatctac	gtattagtca	600
tcgctattac	catggtgatg	cggtttttggc	agtacatcaa	tgggcgtgga	tagcggtttg	660
actcacgggg	atttccaagt	ctccacccca	ttgacgtcaa	tgggagtttg	ttttggcacc	720
aaaatcaacg	ggactttcca	aaatgtcgta	acaactccgc	cccattgacg	caaatggggcg	780
gtaggcgtgt	acgggtgggag	gtctatataa	gcagagctct	ctggctaact	agagaaccca	840
ctgcttactg	gcttatcgaa	attaatacga	ctcactatag	ggagacccaa	gcttggtacc	900
gccgcccgc	atg ggc aag agg tcc gcc ggc tca atc atg tgg ctc gcg agc					951
	Met Gly Lys Arg Ser Ala Gly Ser Ile Met Trp Leu Ala Ser					
	1 5 10					

ttg gca gtt gtc ata gct tgt gca ggc gcc ttc cat tta acc aca cgt	999
Leu Ala Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg	

15	20	25	30	
aac gga gaa cca cac atg atc gtc agc aga caa gag aaa ggg aaa agt				1047
Asn Gly Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser	35	40	45	
ctt ctg ttt aaa aca gag gat ggc gtg aac atg tgt acc ctc atg gcc				1095
Leu Leu Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala	50	55	60	
atg gac ctt ggt gaa ttg tgt gaa gac aca atc acg tac aag tgt ccc				1143
Met Asp Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro	65	70	75	
ctt ctc agg cag aat gag cca gaa gac ata gac tgt tgg tgc aac tct				1191
Leu Leu Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser	80	85	90	
acg tcc acg tgg gta act tat ggg acg tgt acc acc atg gga gaa cat				1239
Thr Ser Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His	95	100	105	110
aga aga gaa aaa aga tca gtg gca ctc gtt cca cat gtg gga atg gga				1287
Arg Arg Glu Lys Arg Ser Val Ala Leu Val Pro His Val Gly Met Gly	115	120	125	
ctg gag aca cga act gaa aca tgg atg tca tca gaa ggg gcc tgg aaa				1335
Leu Glu Thr Arg Thr Glu Thr Trp Met Ser Ser Glu Gly Ala Trp Lys	130	135	140	
cat gtc cag aga att gaa act tgg atc ttg aga cat cca ggc ttc acc				1383
His Val Gln Arg Ile Glu Thr Trp Ile Leu Arg His Pro Gly Phe Thr	145	150	155	
atg atg gca gca atc ctg gca tac acc ata gga acg aca cat ttc caa				1431
Met Met Ala Ala Ile Leu Ala Tyr Thr Ile Gly Thr Thr His Phe Gln	160	165	170	
aga gcc ctg att ttc atc tta ctg aca gct gtc act cct tca atg aca				1479
Arg Ala Leu Ile Phe Ile Leu Leu Thr Ala Val Thr Pro Ser Met Thr	175	180	185	190
atg cgt tgc ata gga atg tca aat aga gac ttt gtg gaa ggg gtt tca				1527
Met Arg Cys Ile Gly Met Ser Asn Arg Asp Phe Val Glu Gly Val Ser	195	200	205	
gga gga agc tgg gtt gac ata gtc tta gaa cat gga agc tgt gtg acg				1575
Gly Gly Ser Trp Val Asp Ile Val Leu Glu His Gly Ser Cys Val Thr	210	215	220	
acg atg gca aaa aac aaa cca aca ttg gat ttt gaa ctg ata aaa aca				1623
Thr Met Ala Lys Asn Lys Pro Thr Leu Asp Phe Glu Leu Ile Lys Thr	225	230	235	
gaa gcc aaa cag cct gcc acc cta agg aag tac tgt ata gag gca aag				1671
Glu Ala Lys Gln Pro Ala Thr Leu Arg Lys Tyr Cys Ile Glu Ala Lys	240	245	250	

cta acc aac aca aca aca gaa tct cgc tgc cca aca caa ggg gaa ccc	1719
Leu Thr Asn Thr Thr Thr Glu Ser Arg Cys Pro Thr Gln Gly Glu Pro	
255 260 265 270	
agc cta aat gaa gag cag gac aaa agg ttc gtc tgc aaa cac tcc atg	1767
Ser Leu Asn Glu Glu Gln Asp Lys Arg Phe Val Cys Lys His Ser Met	
275 280 285	
gta gac aga gga tgg gga aat gga tgt gga cta ttt gga aag gga ggc	1815
Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Gly	
290 295 300	
att gtg acc tgt gct atg ttc aga tgc aaa aag aac atg gaa gga aaa	1863
Ile Val Thr Cys Ala Met Phe Arg Cys Lys Lys Asn Met Glu Gly Lys	
305 310 315	
gtt gtg caa cca gaa aac ttg gaa tac acc att gtg ata aca cct cac	1911
Val Val Gln Pro Glu Asn Leu Glu Tyr Thr Ile Val Ile Thr Pro His	
320 325 330	
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Phe Asn Glu Met Val Leu Leu Gln Met Glu Asn Lys Ala Trp Leu Val	
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His Arg Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Leu Pro Gly Ala	
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<211> 685

<212> PRT

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<220>

<223> Description of artificial sequence; note =
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 35             40             45
Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala Met Asp
 50             55             60

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Gln	Trp	Phe	Leu	Asp	Leu	Pro	Leu	Pro	Trp	Leu	Pro	Gly	Ala	Asp	Thr
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Pro	His	Ala	Lys	Lys	Gln	Asp	Val	Val	Val	Leu	Gly	Ser	Gln	Glu	Gly
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Arg	Val	Gln	Tyr	Glu	Gly	Asp	Gly	Ser	Pro	Cys	Lys	Ile	Pro	Phe	Glu

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<210> 45

<211> 685

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<400> 45

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Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser Leu Leu
      35             40             45
Phe Lys Thr Glu Asp Gly Val Asn Met Cys Thr Leu Met Ala Met Asp
      50             55             60
Leu Gly Glu Leu Cys Glu Asp Thr Ile Thr Tyr Lys Cys Pro Leu Leu
65             70             75             80
Arg Gln Asn Glu Pro Glu Asp Ile Asp Cys Trp Cys Asn Ser Thr Ser
      85             90             95
Thr Trp Val Thr Tyr Gly Thr Cys Thr Thr Met Gly Glu His Arg Arg

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58

Pro Pro Phe Gly Asp Ser His Ile Ile Ile Gly Val Glu Pro Gly Gln
565 570 575
Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Ser Ile Gly Gln Met Phe
580 585 590
Glu Thr Thr Met Arg Gly Ala Lys Arg Met Ala Ile Leu Gly Asp Thr
595 600 605

Ala Trp Asp Phe Gly Ser Leu Gly Gly Val Phe Thr Ser Ile Gly Lys
610 615 620
Ala Leu His Gln Val Phe Gly Gly Ala Phe Arg Thr Leu Phe Gly Gly
625 630 635 640
Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu Trp Met
645 650 655
Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu Ala Thr
660 665 670
Gly Gly Val Leu Val Phe Leu Ala Thr Asn Val His Ala
675 680 685

<210> 46
<211> 5293
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of artificial sequence; note =
synthetic construct

<221> CDS
<222> (910) ... (2964)

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cccgccatt gacgtcaata atgacgtatg ttcccatagt aacgccaata gggactttcc 420
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tcgctattac catggtgatg cggttttggc agtacatcaa tgggcgtgga tagcggtttg 660
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1 5 10
ttg gca gtt gtc ata gct tgt gca ggc gcc ttc cat tta acc aca cgt 999
Leu Ala Val Val Ile Ala Cys Ala Gly Ala Phe His Leu Thr Thr Arg
15 20 25 30

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Asn Gly Glu Pro His Met Ile Val Ser Arg Gln Glu Lys Gly Lys Ser

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Leu	Leu	Phe	Lys	Thr	Glu	Asp	Gly	Val	Asn	Met	Cys	Thr	Leu	Met	Ala					
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Met	Asp	Leu	Gly	Glu	Leu	Cys	Glu	Asp	Thr	Ile	Thr	Tyr	Lys	Cys	Pro					
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ctt	ctc	agg	cag	aat	gag	cca	gaa	gac	ata	gac	tgt	tgg	tgc	aac	tct	1191				
Leu	Leu	Arg	Gln	Asn	Glu	Pro	Glu	Asp	Ile	Asp	Cys	Trp	Cys	Asn	Ser					
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acg	tcc	acg	tgg	gta	act	tat	ggg	acg	tgt	acc	acc	atg	gga	gaa	cat	1239				
Thr	Ser	Thr	Trp	Val	Thr	Tyr	Gly	Thr	Cys	Thr	Thr	Met	Gly	Glu	His					
	95				100				105					110						
aga	aga	gaa	aaa	aga	tca	gtg	gca	ctc	gtt	cca	cat	gtg	gga	atg	gga	1287				
Arg	Arg	Glu	Lys	Arg	Ser	Val	Ala	Leu	Val	Pro	His	Val	Gly	Met	Gly					
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ctg	gag	aca	cga	act	gaa	aca	tgg	atg	tca	tca	gaa	ggg	gcc	tgg	aaa	1335				
Leu	Glu	Thr	Arg	Thr	Glu	Thr	Trp	Met	Ser	Ser	Glu	Gly	Ala	Trp	Lys					
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cat	gtc	cag	aga	att	gaa	act	tgg	atc	ttg	aga	cat	cca	ggc	ttc	acc	1383				
His	Val	Gln	Arg	Ile	Glu	Thr	Trp	Ile	Leu	Arg	His	Pro	Gly	Phe	Thr					
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Met	Met	Ala	Ala	Ile	Leu	Ala	Tyr	Thr	Ile	Gly	Thr	Thr	His	Phe	Gln					
		160				165					170									
aga	gcc	ctg	att	ttc	atc	tta	ctg	aca	gct	gtc	act	cct	tca	atg	aca	1479				
Arg	Ala	Leu	Ile	Phe	Ile	Leu	Leu	Thr	Ala	Val	Thr	Pro	Ser	Met	Thr					
	175				180				185					190						
atg	cgt	tgc	ata	gga	atg	tca	aat	aga	gac	ttt	gtg	gaa	ggg	gtt	tca	1527				
Met	Arg	Cys	Ile	Gly	Met	Ser	Asn	Arg	Asp	Phe	Val	Glu	Gly	Val	Ser					
			195					200						205						
gga	gga	agc	tgg	gtt	gac	ata	gtc	tta	gaa	cat	ggg	agc	tgt	gtg	acg	1575				
Gly	Gly	Ser	Trp	Val	Asp	Ile	Val	Leu	Glu	His	Gly	Ser	Cys	Val	Thr					
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acg	atg	gca	aaa	aac	aaa	cca	aca	ttg	gat	ttt	gaa	ctg	ata	aaa	aca	1623				
Thr	Met	Ala	Lys	Asn	Lys	Pro	Thr	Leu	Asp	Phe	Glu	Leu	Ile	Lys	Thr					
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gaa	gcc	aaa	cag	cct	gcc	acc	cta	agg	aag	tac	tgt	ata	gag	gca	aag	1671				
Glu	Ala	Lys	Gln	Pro	Ala	Thr	Leu	Arg	Lys	Tyr	Cys	Ile	Glu	Ala	Lys					
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cta	acc	aac	aca	aca	aca	gaa	tct	cgc	tgc	cca	aca	caa	ggg	gaa	ccc	1719				

Leu	Thr	Asn	Thr	Thr	Thr	Glu	Ser	Arg	Cys	Pro	Thr	Gln	Gly	Glu	Pro	
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Ser	Leu	Asn	Glu	Glu	Gln	Asp	Lys	Arg	Phe	Val	Cys	Lys	His	Ser	Met	
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Val	Val	Gln	Pro	Glu	Asn	Leu	Glu	Tyr	Thr	Ile	Val	Ile	Thr	Pro	His	
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Phe	Asn	Glu	Met	Val	Leu	Leu	Gln	Met	Glu	Asn	Lys	Ala	Trp	Leu	Val	
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His	Arg	Gln	Trp	Phe	Leu	Asp	Leu	Pro	Leu	Pro	Trp	Leu	Pro	Gly	Ala	
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Lys	Asn	Pro	His	Ala	Lys	Lys	Gln	Asp	Val	Val	Val	Leu	Gly	Ser	Gln	
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Glu	Gly	Ala	Met	His	Thr	Ala	Leu	Thr	Gly	Ala	Thr	Glu	Ile	Gln	Met	
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tca	tca	gga	aac	tta	ctc	ttc	aca	gga	cat	ctc	aag	tgc	agg	ctg	aga	2343
Ser	Ser	Gly	Asn	Leu	Leu	Phe	Thr	Gly	His	Leu	Lys	Cys	Arg	Leu	Arg	
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Lys Phe Lys Val Val Lys Glu Ile Ala Glu Thr Gln His Gly Thr Ile	
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gtt atc aga gtg caa tat gaa ggg gac ggc tct cca tgc aag atc cct	2487
Val Ile Arg Val Gln Tyr Glu Gly Asp Gly Ser Pro Cys Lys Ile Pro	
515 520 525	
ttt gag ata atg gat ttg gaa aaa aga cat gtc tta ggt cgc ctg att	2535
Phe Glu Ile Met Asp Leu Glu Lys Arg His Val Leu Gly Arg Leu Ile	
530 535 540	
aca gtc aac cca att gtg aca gaa aaa gat agc cca gtc aac ata gaa	2583
Thr Val Asn Pro Ile Val Thr Glu Lys Asp Ser Pro Val Asn Ile Glu	
545 550 555	
gca gaa cct cca ttc gga gac agc tac atc atc ata gga gta gag ccg	2631
Ala Glu Pro Pro Phe Gly Asp Ser Tyr Ile Ile Ile Gly Val Glu Pro	
560 565 570	
gga caa ctg aag ctc aac tgg ttt aag aaa gga agc acg ctg ggc aag	2679
Gly Gln Leu Lys Leu Asn Trp Phe Lys Lys Gly Ser Thr Leu Gly Lys	
575 580 585 590	
gcc ttt tca aca act ttg aag gga gct caa aga ctg gca gcg ttg ggc	2727
Ala Phe Ser Thr Thr Leu Lys Gly Ala Gln Arg Leu Ala Ala Leu Gly	
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gac aca gcc tgg gac ttt ggc tct att gga ggg gtc ttc aac tcc ata	2775
Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Asn Ser Ile	
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Gly Gly Met Ser Trp Ile Thr Gln Gly Leu Met Gly Ala Leu Leu Leu	
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Trp Met Gly Val Asn Ala Arg Asp Arg Ser Ile Ala Leu Ala Phe Leu	
655 660 665 670	
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<210> 47

<211> 685

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<400> 47

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			20					25					30		
Glu	Pro	His	Met	Ile	Val	Ser	Arg	Gln	Glu	Lys	Gly	Lys	Ser	Leu	Leu
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Phe	Lys	Thr	Glu	Asp	Gly	Val	Asn	Met	Cys	Thr	Leu	Met	Ala	Met	Asp
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Leu	Gly	Glu	Leu	Cys	Glu	Asp	Thr	Ile	Thr	Tyr	Lys	Cys	Pro	Leu	Leu
65					70					75				80	

Arg	Gln	Asn	Glu	Pro	Glu	Asp	Ile	Asp	Cys	Trp	Cys	Asn	Ser	Thr	Ser
				85					90					95	
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			100					105					110		
Glu	Lys	Arg	Ser	Val	Ala	Leu	Val	Pro	His	Val	Gly	Met	Gly	Leu	Glu
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Thr	Arg	Thr	Glu	Thr	Trp	Met	Ser	Ser	Glu	Gly	Ala	Trp	Lys	His	Val
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Gln	Arg	Ile	Glu	Thr	Trp	Ile	Leu	Arg	His	Pro	Gly	Phe	Thr	Met	Met
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Ala	Ala	Ile	Leu	Ala	Tyr	Thr	Ile	Gly	Thr	Thr	His	Phe	Gln	Arg	Ala
				165					170					175	
Leu	Ile	Phe	Ile	Leu	Leu	Thr	Ala	Val	Thr	Pro	Ser	Met	Thr	Met	Arg
			180					185					190		
Cys	Ile	Gly	Met	Ser	Asn	Arg	Asp	Phe	Val	Glu	Gly	Val	Ser	Gly	Gly
	195						200					205			
Ser	Trp	Val	Asp	Ile	Val	Leu	Glu	His	Gly	Ser	Cys	Val	Thr	Thr	Met
	210					215					220				
Ala	Lys	Asn	Lys	Pro	Thr	Leu	Asp	Phe	Glu	Leu	Ile	Lys	Thr	Glu	Ala
225					230					235					240
Lys	Gln	Pro	Ala	Thr	Leu	Arg	Lys	Tyr	Cys	Ile	Glu	Ala	Lys	Leu	Thr
				245					250					255	
Asn	Thr	Thr	Thr	Glu	Ser	Arg	Cys	Pro	Thr	Gln	Gly	Glu	Pro	Ser	Leu
			260					265				270			
Asn	Glu	Glu	Gln	Asp	Lys	Arg	Phe	Val	Cys	Lys	His	Ser	Met	Val	Asp
	275						280					285			
Arg	Gly	Trp	Gly	Asn	Gly	Cys	Gly	Leu	Phe	Gly	Lys	Gly	Gly	Ile	Val
	290					295					300				
Thr	Cys	Ala	Met	Phe	Arg	Cys	Lys	Lys	Asn	Met	Glu	Gly	Lys	Val	Val
305					310					315					320
Gln	Pro	Glu	Asn	Leu	Glu	Tyr	Thr	Ile	Val	Ile	Thr	Pro	His	Ser	Gly
				325					330					335	
Glu	Glu	His	Ala	Val	Gly	Asn	Asp	Thr	Gly	Lys	His	Gly	Lys	Glu	Ile
			340					345					350		
Lys	Ile	Thr	Pro	Gln	Ser	Ser	Ile	Thr	Glu	Ala	Glu	Leu	Thr	Gly	Tyr
	355						360					365			
Gly	Thr	Val	Thr	Met	Glu	Cys	Ser	Pro	Arg	Thr	Gly	Leu	Asp	Phe	Asn
	370					375					380				
Glu	Met	Val	Leu	Leu	Gln	Met	Glu	Asn	Lys	Ala	Trp	Leu	Val	His	Arg
385					390					395					400
Gln	Trp	Phe	Leu	Asp	Leu	Pro	Leu	Pro	Trp	Leu	Pro	Gly	Ala	Asp	Thr
				405					410					415	
Gln	Gly	Ser	Asn	Trp	Ile	Gln	Lys	Glu	Thr	Leu	Val	Thr	Phe	Lys	Asn
			420					425					430		
Pro	His	Ala	Lys	Lys	Gln	Asp</									

530		535		540
Asn Pro Ile Val Thr	Glu Lys Asp Ser Pro	Val Asn Ile Glu Ala Glu		
545	550	555	560	
Pro Pro Phe Gly Asp	Ser Tyr Ile Ile Ile	Gly Val Glu Pro Gly Gln		
	565	570	575	
Leu Lys Leu Asn Trp	Phe Lys Lys Gly Ser Thr	Leu Gly Lys Ala Phe		
	580	585	590	
Ser Thr Thr Leu Lys	Gly Ala Gln Arg Leu Ala Ala	Leu Gly Asp Thr		
	595	600	605	
Ala Trp Asp Phe Gly	Ser Ile Gly Gly Val Phe Asn Ser	Ile Gly Lys		
	610	615	620	
Ala Val His Gln Val	Phe Gly Gly Ala Phe Arg Thr	Leu Phe Gly Gly		
625	630	635	640	
Met Ser Trp Ile Thr	Gln Gly Leu Met Gly Ala Leu Leu Leu	Trp Met		
	645	650	655	
Gly Val Asn Ala Arg	Asp Arg Ser Ile Ala Leu Ala Phe	Leu Ala Thr		
	660	665	670	
Gly Gly Val Leu Val	Phe Leu Ala Thr Asn Val His Ala			
	675	680	685	

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<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of artificial sequence; note =
synthetic construct

<400> 48

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34

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<213> Artificial Sequence

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40

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<212> DNA

<213> Artificial Sequence

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30

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 <210> 52
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 <213> Artificial Sequence

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 <210> 53
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 <213> Artificial Sequence

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<210> 56
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 <213> Artificial Sequence

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 synthetic construct

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33

<210> 61
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1 5 10